

J. Woitach

#7
RP
11-24-00

1632

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/509,738

DATE: 11/02/2000
TIME: 10:31:05

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NOV 14 2000

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3 <110> APPLICANT: PLANT BIOSCIENCE LIMITED
5 <120> TITLE OF INVENTION: PROTEIN
7 <130> FILE REFERENCE: P001201
C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/509,738
C--> 10 <141> CURRENT FILING DATE: 2000-05-24
12 <160> NUMBER OF SEQ ID NOS: 5
14 <170> SOFTWARE: PatentIn Ver. 2.1
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 1205
18 <212> TYPE: DNA
19 <213> ORGANISM: Arabidopsis thaliana
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30 ttc aga gct gac gat caa tcg gac tct cac gcc ata gaa atg gga gac 98
31 Phe Arg Ala Asp Asp Gln Ser Asp Ser His Ala Ile Glu Met Gly Asp
32 15 20 25
34 att act ggc gga gtc aat ctc gac aaa ttc ttc gaa gat gtt gaa gcc 146
35 Ile Thr Gly Gly Val Asn Leu Asp Lys Phe Phe Glu Asp Val Glu Ala
36 30 35 40
38 att aaa gac gaa ctc aaa ggc ctc gag aaa atc tat tcc caa ctc caa 194
39 Ile Lys Asp Glu Leu Lys Gly Leu Glu Lys Ile Tyr Ser Gln Leu Gln
40 45 50 55
42 tct tcc cat gaa aaa agc aag act ctt cac aac gct aaa gcc gtt aaa 242
43 Ser Ser His Glu Lys Ser Lys Thr Leu His Asn Ala Lys Ala Val Lys
44 60 65 70 75
46 gat cta aga tcc aac atg gat aat gac gtt tcc atg gca ttg aag aaa 290
47 Asp Leu Arg Ser Asn Met Asp Asn Asp Val Ser Met Ala Leu Lys Lys
48 80 85 90
50 gcc aaa ttc atc aaa gtt cgt ctc gaa gcc tta gac aga tca aat gca 338
51 Ala Lys Phe Ile Lys Val Arg Leu Glu Ala Leu Asp Arg Ser Asn Ala
52 95 100 105
54 gcg aat cga agc ctc cct gga tgt gga ccc gga agt tca tct gac agg 386
55 Ala Asn Arg Ser Leu Pro Gly Cys Gly Pro Gly Ser Ser Ser Asp Arg
56 110 115 120
58 acg aga act tca gtt gtg aac gga tta agg aag aaa ctt caa gag tca 434
59 Thr Arg Thr Ser Val Val Asn Gly Leu Arg Lys Lys Leu Gln Glu Ser
60 125 130 135
62 atg aat cag ttc aac gag cta agg caa aag atg gca tct gaa tat agg 482
63 Met Asn Gln Phe Asn Glu Leu Arg Gln Lys Met Ala Ser Glu Tyr Arg
64 140 145 150 155
66 gaa aca gtt caa cga cga tat tat acc gtc aca gga gaa aat cct gat 530
67 Glu Thr Val Gln Arg Arg Tyr Tyr Thr Val Thr Gly Glu Asn Pro Asp

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70 gaa gca gtt ctt gat aca ctc ata tct aca ggt caa agt gag acg ttc 578
71 Glu Ala Val Leu Asp Thr Leu Ile Ser Thr Gly Gln Ser Glu Thr Phe
72          175          180          185
74 ttg caa aag gca att caa gag caa ggg aga gga caa gtg atg gat aca 626
75 Leu Gln Lys Ala Ile Gln Glu Gln Gly Arg Gly Gln Val Met Asp Thr
76          190          195          200
78 gtt atg gaa att caa gaa agg cat gaa gct gtg aag gaa ttg gag agg 674
79 Val Met Glu Ile Gln Glu Arg His Glu Ala Val Lys Glu Leu Glu Arg
80          205          210          215
82 aat ttg aaa gaa ttg cat caa gta ttc ttg gac atg gct gtt ttg gtt 722
83 Asn Leu Lys Glu Leu His Gln Val Phe Leu Asp Met Ala Val Leu Val
84 220          225          230          235
86 gaa agt caa gga gct caa ctt gat gat att gag agc caa gtg aat agg 770
87 Glu Ser Gln Gly Ala Gln Leu Asp Asp Ile Glu Ser Gln Val Asn Arg
88          240          245          250
90 gct aat tcc ttc gtt aga ggg ggt gct cag caa ctg caa gtg gca agg 818
91 Ala Asn Ser Phe Val Arg Gly Gly Ala Gln Gln Leu Gln Val Ala Arg
92          255          260          265
94 aag cac cag aag aac act aga aaa tgg act tgt ttt gct att att ctt 866
95 Lys His Gln Lys Asn Thr Arg Lys Trp Thr Cys Phe Ala Ile Ile Leu
96          270          275          280
98 ctg ctt atc atc att ttg gtg gtt gtt ctt tct att cag cca tgg aaa 914
99 Leu Leu Ile Ile Ile Leu Val Val Val Leu Ser Ile Gln Pro Trp Lys
100          285          290          295
102 aaa tgagaatttg tctatggtca aaggtcttct ggtggacccc ttcaatgttt 967
103 Lys
104 300
106 tgaatattct aaatttttat attttattat tttagccatg cttattattt tgtgttattt 1027
108 tggatttttt tttgtttttt aatgtgggga agagtaaaact ggatgggggt ccatgtgcta 1087
110 tttagagaaa tacttgggag ttctcttttt gtaattattg ctgtatttag agtataattc 1147
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125 20 25 30
127 Asn Leu Asp Lys Phe Phe Glu Asp Val Glu Ala Ile Lys Asp Glu Leu
128 35 40 45
130 Lys Gly Leu Glu Lys Ile Tyr Ser Gln Leu Gln Ser Ser His Glu Lys
131 50 55 60
133 Ser Lys Thr Leu His Asn Ala Lys Ala Val Lys Asp Leu Arg Ser Asn
134 65 70 75 80
136 Met Asp Asn Asp Val Ser Met Ala Leu Lys Lys Ala Lys Phe Ile Lys
137 85 90 95

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142 Pro Gly Cys Gly Pro Gly Ser Ser Ser Asp Arg Thr Arg Thr Ser Val
143      115      120      125
145 Val Asn Gly Leu Arg Lys Lys Leu Gln Glu Ser Met Asn Gln Phe Asn
146      130      135      140
148 Glu Leu Arg Gln Lys Met Ala Ser Glu Tyr Arg Glu Thr Val Gln Arg
149 145      150      155      160
151 Arg Tyr Tyr Thr Val Thr Gly Glu Asn Pro Asp Glu Ala Val Leu Asp
152      165      170      175
154 Thr Leu Ile Ser Thr Gly Gln Ser Glu Thr Phe Leu Gln Lys Ala Ile
155      180      185      190
157 Gln Glu Gln Gly Arg Gly Gln Val Met Asp Thr Val Met Glu Ile Gln
158      195      200      205
160 Glu Arg His Glu Ala Val Lys Glu Leu Glu Arg Asn Leu Lys Glu Leu
161      210      215      220
163 His Gln Val Phe Leu Asp Met Ala Val Leu Val Glu Ser Gln Gly Ala
164 225      230      235      240
166 Gln Leu Asp Asp Ile Glu Ser Gln Val Asn Arg Ala Asn Ser Phe Val
167      245      250      255
169 Arg Gly Gly Ala Gln Gln Leu Gln Val Ala Arg Lys His Glu Lys Asn
170      260      265      270
172 Thr Arg Lys Trp Thr Cys Phe Ala Ile Ile Leu Leu Leu Ile Ile Ile
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193      Met Asn Asp Leu Phe Ser Ser Ser Phe Ser Arg Phe
194      1      5      10
196 cgc agc gga gaa cca tcc cct cgc cga gac gtt gcc ggc ggt ggc gac 160
197 Arg Ser Gly Glu Pro Ser Pro Arg Arg Asp Val Ala Gly Gly Gly Asp
198      15      20      25
200 gga gtt cag atg gcg aat ccc gcg gga tca acc ggt ggt gtg aac ctc 208
201 Gly Val Gln Met Ala Asn Pro Ala Gly Ser Thr Gly Gly Val Asn Leu
202      30      35      40
204 gac aag ttc ttc gaa gat gtt gaa tct gtg aaa gaa gag cta aag gag 256
205 Asp Lys Phe Phe Glu Asp Val Glu Ser Val Lys Glu Glu Leu Lys Glu
206 45      50      55      60
208 cta gat cgg ctc aac gaa aca ctc tct tca tgt cac gag cag agc aag 304
209 Leu Asp Arg Leu Asn Glu Thr Leu Ser Ser Cys His Glu Gln Ser Lys

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213	Thr Leu His Asn Ala Lys Ala Val Lys Asp Leu Arg Ser Lys Met Asp			
214	80 85 90			
216	ggt gac gtt gga gtc gcg ttg aag aag gcg aag atg att aaa gtt aaa	400		
217	Gly Asp Val Gly Val Ala Leu Lys Lys Ala Lys Met Ile Lys Val Lys			
218	95 100 105			
220	ctc gag gcg cta gat cgt gcc aat gct gct aat cgg agt ctc cct ggc	448		
221	Leu Glu Ala Leu Asp Arg Ala Asn Ala Ala Asn Arg Ser Leu Pro Gly			
222	110 115 120			
224	tgt gga cct ggt tct tcc tcc gat cga acc agg acc tct gtc ctc aat	496		
225	Cys Gly Pro Gly Ser Ser Ser Ser Arg Thr Arg Thr Ser Val Leu Asn			
226	125 130 135 140			
228	ggt ctc agg aag aaa ttg atg gac tct atg gat agt ttc aac cga ttg	544		
229	Gly Leu Arg Lys Lys Leu Met Asp Ser Met Asp Ser Phe Asn Arg Leu			
230	145 150 155			
232	agg gag ctt atc tcg tcc gag tat aqa gaa act gta cag agg agg tac	592		
233	Arg Glu Leu Ile Ser Ser Glu Tyr Arg Glu Thr Val Gln Arg Arg Tyr			
234	160 165 170			
236	ttc acc gtc acc gcc gag aat ccg gat gaa cga acc cta gat cga ctg	640		
237	Phe Thr Val Thr Gly Glu Asn Pro Asp Glu Arg Thr Leu Asp Arg Leu			
238	175 180 185			
240	att tcc act gga gag agt gag aga ttc ttg cag aaa gca ata caa gaa	688		
241	Ile Ser Thr Gly Glu Ser Glu Arg Phe Leu Gln Lys Ala Ile Gln Glu			
242	190 195 200			
244	caa gga aga gga agg gtg tta gac acc att aac gag att caa gaa agg	736		
245	Gln Gly Arg Gly Arg Val Leu Asp Thr Ile Asn Glu Ile Gln Glu Arg			
246	205 210 215 220			
248	cat gat gcg gtt aaa gac att gag aag aat ctc agg gag ctt cac cag	784		
249	His Asp Ala Val Lys Asp Ile Glu Lys Asn Leu Arg Glu Leu His Gln			
250	225 230 235			
252	gtg ttt cta gac atg gcc gtg ctg gta gag cac cag gga gct cag ctt	832		
253	Val Phe Leu Asp Met Ala Val Leu Val Glu His Gln Gly Ala Gln Leu			
254	240 245 250			
256	gat gac atc gag agt cat gtg ggt cga gct agc tcc ttt atc aga gcc	880		
257	Asp Asp Ile Glu Ser His Val Gly Arg Ala Ser Ser Phe Ile Arg Gly			
258	255 260 265			
260	gga act gac cag cta caa acc gct cgg gtt tac cag aag aac acg cga	928		
261	Gly Thr Asp Gln Leu Gln Thr Ala Arg Val Tyr Gln Lys Asn Thr Arg			
262	270 275 280			
264	aaa tgg aca tgt att gcc att att att ctc atc atc atc ata act gtt	976		
265	Lys Trp Thr Cys Ile Ala Ile Ile Ile Leu Ile Ile Ile Thr Val			
266	285 290 295 300			
268	gtg gtt ctt gct gtt ttaaaaccgt ggaacaacag cagtggcggc ggcggcggty	1031		
269	Val Val Leu Ala Val			
270	305			
272	gtgggtggtgg ggggtaccact ggaggaagtc aaccaaattc agggacacca ccaaattctc	1091		
274	ctcaggcaag gcgtctattg cgttgaagtt gaagttgaag ttgagtttcg ttatttgcac	1151		
276	atatattctt tclttgaaaa accctatttat caaaccagct ttgtgttact acctttctact	1211		

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Input Set : A:\P0012011.app
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287 <212> TYPE: PRT
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297 Ala Asn Pro Ala Gly Ser Thr Gly Gly Val Asn Leu Asp Lys Phe Phe
298 35 40 45
300 Glu Asp Val Glu Ser Val Lys Glu Glu Leu Lys Glu Leu Asp Arg Leu
301 50 55 60
303 Asn Glu Thr Leu Ser Ser Cys His Glu Gln Ser Lys Thr Leu His Asn
304 65 70 75 80
306 Ala Lys Ala Val Lys Asp Leu Arg Ser Lys Met Asp Gly Asp Val Gly
307 85 90 95
309 Val Ala Leu Lys Lys Ala Lys Met Ile Lys Val Lys Leu Glu Ala Leu
310 100 105 110
312 Asp Arg Ala Asn Ala Ala Asn Arg Ser Leu Pro Gly Cys Gly Pro Gly
313 115 120 125
315 Ser Ser Ser Asp Arg Thr Arg Thr Ser Val Leu Asn Gly Leu Arg Lys
316 130 135 140
318 Lys Leu Met Asp Ser Met Asp Ser Phe Asn Arg Leu Arg Glu Leu Ile
319 145 150 155 160
321 Ser Ser Glu Tyr Arg Glu Thr Val Gln Arg Arg Tyr Phe Thr Val Thr
322 165 170 175
324 Gly Glu Asn Pro Asp Glu Arg Thr Leu Asp Arg Leu Ile Ser Thr Gly
325 180 185 190
327 Glu Ser Glu Arg Phe Leu Gln Lys Ala Ile Gln Glu Gln Gly Arg Gly
328 195 200 205
330 Arg Val Leu Asp Thr Ile Asn Glu Ile Gln Glu Arg His Asp Ala Val
331 210 215 220
333 Lys Asp Ile Glu Lys Asn Leu Arg Glu Leu His Gln Val Phe Leu Asp
334 225 230 235 240
336 Met Ala Val Leu Val Glu His Gln Gly Ala Gln Leu Asp Asp Ile Glu
337 245 250 255
339 Ser His Val Gly Arg Ala Ser Ser Phe Ile Arg Gly Gly Thr Asp Gln
340 260 265 270
342 Leu Gln Thr Ala Arg Val Tyr Gln Lys Asn Thr Arg Lys Trp Thr Cys
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346 290 295 300
348 Val
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VERIFICATION SUMMARY DATE: 11/02/2000
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L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date